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 NEWS 12  Apr 17   Polymer searching in REGISTRY enhanced
 NEWS 13  Jun 13   Indexing from 1947 to 1956 added to records in CA/CAPLUS
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                   WPIDS/WPINDEX/WPIX
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 NEWS 18  May 15   Supporter information for ENCOMPPAT and ENCOMPLIT updated
 NEWS 19  May 19   Simultaneous left and right truncation added to WSCA
 NEWS 20  May 19   RAPRA enhanced with new search field, simultaneous left and
                   right truncation
 NEWS 21  Jun 06   Simultaneous left and right truncation added to CBNB
 NEWS 22  Jun 06   PASCAL enhanced with additional data
 NEWS 23  Jun 20   2003 edition of the FSTA Thesaurus is now available
 NEWS 24  Jun 25   HSDB has been reloaded

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L1 54 CIPHERGEN

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L2 ANSWER 1 OF 46 MEDLINE
AN 2003309657 IN-PROCESS
DN 22721803 PubMed ID: 12837598
TI Use of proteinchip array surface enhanced laser desorption/ionization time-of-flight mass spectrometry (seldi-tof ms) to identify thymosin beta-4, a differentially secreted protein from lymphoblastoid cell lines.
AU Diamond Deborah L; Zhang Yanni; Gaiger Alexander; Smithgall Molly; Vedvick Thomas S; Carter Darrick
CS Ciphergen Biosystems Inc., Fremont, California, USA.
SO JOURNAL OF THE AMERICAN SOCIETY FOR MASS SPECTROMETRY, (2003 Jul) 14 (7) 760-5.
Journal code: 9010412. ISSN: 1044-0305.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS IN-PROCESS; NONINDEXED; Priority Journals
ED Entered STN: 20030703
Last Updated on STN: 20030703
AB The identification of proteins differentially expressed between cancer and normal cells is vital for the development of cancer diagnostics, therapeutics and vaccines. Using a ProteinChip Biomarker System (**Ciphergen** Biosystems, Fremont, CA) which combines ProteinChip technology with time-of-flight mass spectrometry, we have developed a simple method to screen and identify differentially secreted proteins from tumor cell lines. Mass spectra of the range of proteins secreted from normal B-cells were generated along with those secreted from Epstein-Barr virus transformed B-cells. A mass peak at m/z = 4972.1 that was highly over-represented in the transformed B-cell line was chosen for identification and purified by reversed phase chromatography with concomitant monitoring of fractions by SELDI-TOF MS. The resulting purified protein was digested with trypsin and the peptide masses derived from the SELDI-TOF spectrum were used to search the public databases for protein identification. Fragment matching of the resulting peptides identified the protein as thymosin beta-4. Using LC-electrospray ionization MS/MS, the identity of this protein was confirmed. Thymosin beta-4 is a known marker in LCLs establishing the utility of this method to discover and identify proteins differentially expressed between cancers and their matched normal counterparts.

L2 ANSWER 2 OF 46 MEDLINE

AN 2003204149 MEDLINE
DN 22609862 PubMed ID: 12724632
TI Characterization of renal allograft rejection by urinary proteomic analysis.
AU Clarke William; Silverman Benjamin C; Zhang Zhen; Chan Daniel W; Klein Andrew S; Molmenti Ernesto P
CS Department of Surgery, The Johns Hopkins University School of Medicine, 600 North Wolfe Street, Baltimore, MD 21287-8611, USA.
SO ANNALS OF SURGERY, (2003 May) 237 (5) 660-4; discussion 664-5. Journal code: 0372354. ISSN: 0003-4932.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Abridged Index Medicus Journals; Priority Journals
EM 200306
ED Entered STN: 20030502
Last Updated on STN: 20030618
Entered Medline: 20030617
AB OBJECTIVE: To develop a diagnostic method with no morbidity or mortality for the detection of acute renal transplant rejection. SUMMARY BACKGROUND DATA: Rejection constitutes the major impediment to the success of transplantation. Currently available methods, including clinical presentation and biochemical organ function parameters, often fail to detect rejection until late stages of progression. Renal biopsies have associated morbidity and mortality and provide only a limited sample of the organ. METHODS: Thirty-four urine samples were collected from 32 renal transplant patients at various stages posttransplantation. Samples were collected from 17 transplant recipients with acute rejection and 15 patients with no rejection. Samples from patients less than 4 days posttransplant were omitted from data analysis due to the presence of excessive inflammatory response proteins. Rejection status was confirmed by kidney biopsy. Specimens were analyzed in triplicate using SELDI mass spectrometry. The obtained spectra were subjected to bioinformatic analysis using ProPeak as well as CART (Classification and Regression Tree) algorithms to identify rejection biomarker candidates. These candidates were identified by their molecular weight and ranked by their ability to distinguish between nonrejection and rejection based on receiver operating characteristic (ROC) analysis. The candidates with the highest area under the ROC curve (AUC) exhibited the best diagnostic performance. RESULTS: The best candidate biomarkers demonstrated highly successful diagnostic performance: 6.5 kd (AUC = 0.839, P <.0001), 6.7 kd (AUC = 0.839, P <.0001), 6.6 kd (AUC = 0.807, P <.0001), 7.1 kd (AUC = 0.807, P <.0001), and 13.4 kd (AUC = 0.804, P <.0001). A separate analysis using the CART algorithm in the **Ciphergen** Biomarker Pattern Software correctly classified 91% of the 34 specimens in the training set, giving a sensitivity of 83% and specificity of 100% using two separate biomarker candidates at 10.0 kd and 3.4 kd. CONCLUSIONS: Biomarker candidates exist in urine that have the ability to distinguish between renal transplant patients with no rejection and those with acute rejection. These biomarker candidates are the basis for development of a noninvasive method of diagnosing acute rejection without the morbidity and mortality associated with needle biopsy. The combination of biomarkers into a panel for diagnosis leads to the possibility of enhanced diagnostic performance.

L2 ANSWER 3 OF 46 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 2003:150561 BIOSIS
DN PREV200300150561
TI Multifactorial screening design and analysis of SELDI-TOF ProteinChip(R) array optimization experiments.
AU Cordingley, H. C. (1); Roberts, S. L. L.; Tooke, P.; Armitage, J. R.; Lane, P. W.; Wu, W.; Wildsmith, S. E.
CS (1) Safety Assessment, GlaxoSmithKline, The Frythe, Welwyn, Hertfordshire, AL6 9AR, UK: hayley_c_cordingley@gsk.com UK

SO BioTechniques, (February 2003, 2003) Vol. 34, No. 2, pp. 364-373. print.
ISSN: 0736-6205.
DT Article
LA English
AB Surface-enhanced laser desorption/ionization time-of-flight mass spectrometry is a powerful tool for rapidly generating protein expression data (peptide and protein profiles) from a large number of samples. However, as with any technology, it must be optimized and reproducible for one to have confidence in the results. Using a classical statistical method called the fractional factorial design of experiments, we assessed the effects of 11 different experimental factors. We also developed several metrics that reflect trace quality and reproducibility. These were used to measure the effect of each individual factor, and the interactions between factors, to determine optimal factor settings and thus ultimately produce the best possible traces. Significant improvements to output traces were seen by simultaneously altering several parameters, either in the sample preparation procedure or during the matrix preparation and application procedure. This has led to the implementation of an improved method that gives a better quality, reproducible, and robust output.

L2 ANSWER 4 OF 46 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 2003:297046 BIOSIS
DN PREV200300297046
TI The 13th Annual Frederick Conference on capillary electrophoresis.
AU Weinberger, Robert (1)
CS (1) CE Technologies, P. O. Box 140, Chappaqua, NY, 10514, USA: RobertWeinberger@aol.com USA
SO American Biotechnology Laboratory, (January 2003, 2003) Vol. 21, No. 1, pp. 30-31. print.
Meeting Info.: 13th Annual Frederick Conference on Capillary Electrophoresis (CE). Frederick, Maryland, USA October 21-22, 2002
ISSN: 0749-3223.
DT Conference
LA English

L2 ANSWER 5 OF 46 MEDLINE DUPLICATE 1
AN 2002186404 MEDLINE
DN 21909325 PubMed ID: 11912167
TI Identification of hepatocarcinoma-intestine-pancreas/pancreatitis-associated protein I as a biomarker for pancreatic ductal adenocarcinoma by protein biochip technology.
AU Rosty Christophe; Christa Laurence; Kuzdzal Scott; Baldwin William M; Zahurak Marianna L; Carnot Francoise; Chan Daniel W; Canto Marcia; Lillemoe Keith D; Cameron John L; Yeo Charles J; Hruban Ralph H; Goggins Michael
CS Department of Pathology, The Johns Hopkins Medical Institutions, Baltimore, Maryland 21205-2196, USA.
NC P50-CA62924 (NCI)
SO CANCER RESEARCH, (2002 Mar 15) 62 (6) 1868-75.
Journal code: 2984705R. ISSN: 0008-5472.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200204
ED Entered STN: 20020403
Last Updated on STN: 20020430
Entered Medline: 20020429
AB New biomarkers of pancreatic adenocarcinoma are needed to improve the early detection of this deadly disease. We performed surface enhanced laser desorption ionization (SELDI) mass spectrometry using ProteinChip technology (**Ciphergen** Biosystems, Fremont, CA) to screen for differentially expressed proteins in pancreatic juice. Pancreatic juice samples obtained from patients undergoing pancreatectomy for pancreatic

adenocarcinoma were compared with juice samples from patients with other pancreatic diseases. We identified a peak approximately 16,570 daltons present in the pancreatic juice from 10/15 (67%) of the patients with pancreatic adenocarcinoma and in the pancreatic juice from 1/7 (17%) of the patients with other pancreatic diseases. Using a ProteinChip immunoassay, we identified this differentially expressed protein as hepatocarcinoma-intestine-pancreas/pancreatitis-associated-protein I (HIP/PAP-I), a protein released from pancreatic acini during acute pancreatitis and overexpressed in hepatocellular carcinoma. We then quantified by ELISA the pancreatic juice HIP/PAP-I levels in 43 patients (28 with pancreatic adenocarcinoma, 15 with other pancreatic diseases) and the serum HIP/PAP-I levels in 98 patients (53 with pancreatic adenocarcinoma, 45 with other pancreatic diseases or healthy individuals). HIP/PAP-I levels were significantly higher in both the pancreatic juice ($P < 0.001$) and in the serum ($P < 0.001$) of patients with pancreatic adenocarcinoma compared with the control group. HIP/PAP-I levels were approximately 1000-fold higher in pancreatic juice compared with serum and the magnitude of the difference between the pancreatic adenocarcinoma group and the control group was greater in the pancreatic juice samples (143.75 +/- 235.52 microg/ml versus 6.04 +/- 7.59 microg/ml) than in the serum samples (99.96 +/- 140.66 ng/ml versus 35.25 +/- 28.44 ng/ml). In our study, patients with pancreatic juice HIP/PAP-I levels > or= 20 microg/ml were 21.9 times (95% confidence interval, 3.5-136.5; $P < 0.001$) more likely to have pancreatic adenocarcinoma than patients with levels <20 microg/ml. Immunolabeling of tissue sections revealed that the HIP/PAP-I protein was strongly expressed in acini adjacent to the invasive adenocarcinoma, but it was only rarely (1/30; 3%) expressed in the neoplastic epithelium, which suggests that the main source of HIP/PAP-I release in the pancreatic juice is acini. This low level of HIP/PAP-I expression in pancreatic adenocarcinoma was confirmed by reverse transcription-PCR: only 1 (5%) of 19 pancreatic cancer cell lines expressed HIP/PAP-I transcripts. Taken together, these data suggest that pancreatic juice measurement of HIP/PAP-I may help to identify patients with pancreatic adenocarcinoma.

L2 ANSWER 6 OF 46 MEDLINE DUPLICATE 2
AN 2002393504 MEDLINE
DN 22137562 PubMed ID: 12142387
TI Proteomics and bioinformatics approaches for identification of serum biomarkers to detect breast cancer.
AU Li Jinong; Zhang Zhen; Rosenzweig Jason; Wang Young Y; Chan Daniel W
CS Department of Pathology, Johns Hopkins Medical Institutions, Baltimore, MD 21287, USA.
SO CLINICAL CHEMISTRY, (2002 Aug) 48 (8) 1296-304.
Journal code: 9421549. ISSN: 0009-9147.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200208
ED Entered STN: 20020727
Last Updated on STN: 20020806
Entered Medline: 20020805
AB BACKGROUND: Surface-enhanced laser desorption/ionization (SELDI) is an affinity-based mass spectrometric method in which proteins of interest are selectively adsorbed to a chemically modified surface on a biochip, whereas impurities are removed by washing with buffer. This technology allows sensitive and high-throughput protein profiling of complex biological specimens. METHODS: We screened for potential tumor biomarkers in 169 serum samples, including samples from a cancer group of 103 breast cancer patients at different clinical stages [stage 0 (n = 4), stage I (n = 38), stage II (n = 37), and stage III (n = 24)], from a control group of 41 healthy women, and from 25 patients with benign breast diseases. Diluted serum samples were applied to immobilized metal affinity capture

Ciphergen ProteinChip Arrays previously activated with Ni2+. Proteins bound to the chelated metal were analyzed on a ProteinChip Reader Model PBS II. Complex protein profiles of different diagnostic groups were compared and analyzed using the ProPeak software package. RESULTS: A panel of three biomarkers was selected based on their collective contribution to the optimal separation between stage 0-I breast cancer patients and noncancer controls. The same separation was observed using independent test data from stage II-III breast cancer patients. Bootstrap cross-validation demonstrated that a sensitivity of 93% for all cancer patients and a specificity of 91% for all controls were achieved by a composite index derived by multivariate logistic regression using the three selected biomarkers. CONCLUSIONS: Proteomics approaches such as SELDI mass spectrometry, in conjunction with bioinformatics tools, could greatly facilitate the discovery of new and better biomarkers. The high sensitivity and specificity achieved by the combined use of the selected biomarkers show great potential for the early detection of breast cancer.

L2 ANSWER 7 OF 46 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 2002:630094 BIOSIS
DN PREV200200630094
TI Identification of proteomic biomarkers in prostate cancer serum using ProteinChip technology.
AU Li, Xiaohong (1); Fung, Eric; Wright, George; Zhao, Lueping
CS (1) Division of Public Health Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA USA
SO Cancer Epidemiology Biomarkers & Prevention, (October, 2002) Vol. 11, No. 10 Part 2, pp. 1198s. http://cebp.aacrjournals.org/. print.
Meeting Info.: Proceedings of the American Association for Cancer Research Conference on Frontiers in Cancer Prevention Research Boston, MA, USA October 14-18, 2002 American Society of Preventive Oncology
. ISSN: 1055-9965.
DT Conference
LA English

L2 ANSWER 8 OF 46 MEDLINE DUPLICATE 3
AN 2002236889 MEDLINE
DN 21932152 PubMed ID: 11934738
TI An integrated approach utilizing artificial neural networks and SELDI mass spectrometry for the classification of human tumours and rapid identification of potential biomarkers.
AU Ball G; Mian S; Holding F; Allibone R O; Lowe J; Ali S; Li G; McCardle S; Ellis I O; Creaser C; Rees R C
CS Department of Life Sciences, Nottingham Trent University, Clifton Lane, Clifton, Nottingham NG11 8NS, UK.. graham.balls@ntu.ac.uk
SO BIOINFORMATICS, (2002 Mar) 18 (3) 395-404.
Journal code: 9808944. ISSN: 1367-4803.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200209
ED Entered STN: 20020429
Last Updated on STN: 20020921
Entered Medline: 20020920
AB MOTIVATION: MALDI mass spectrometry is able to elicit macromolecular expression data from cellular material and when used in conjunction with **Ciphergen** protein chip technology (also referred to as SELDI-Surface Enhanced Laser Desorption/Ionization), it permits a semi-high throughput approach to be taken with respect to sample processing and data acquisition. Due to the large array of data that is generated from a single analysis (8-10000 variables using a mass range of 2-15 kDa-this paper) it is essential to implement the use of algorithms that can detect expression patterns from such large volumes of data correlating to a given biological/pathological phenotype from multiple

samples. If successful, the methodology could be extrapolated to larger data sets to enable the identification of validated biomarkers correlating strongly to disease progression. This would not only serve to enable tumours to be classified according to their molecular expression profile but could also focus attention upon a relatively small number of molecules that might warrant further biochemical/molecular characterization to assess their suitability as potential therapeutic targets. RESULTS: Using a multi-layer perceptron Artificial Neural Network (ANN) (Neuroshell 2) with a back propagation algorithm we have developed a prototype approach that uses a model system (comprising five low and seven high-grade human astrocytomas) to identify mass spectral peaks whose relative intensity values correlate strongly to tumour grade. Analyzing data derived from MALDI mass spectrometry in conjunction with **Ciphergen** protein chip technology we have used relative importance values, determined from the weights of trained ANNs (Balls et al., Water, Air Soil Pollut., 85, 1467-1472, 1996), to identify masses that accurately predict tumour grade. Implementing a three-stage procedure, we have screened a population of approximately 100000-120000 variables and identified two ions (m/z values of 13454 and 13457) whose relative intensity pattern was significantly reduced in high-grade astrocytoma. The data from this initial study suggests that application of ANN-based approaches can identify molecular ion patterns which strongly associate with disease grade and that its application to larger cohorts of patient material could potentially facilitate the rapid identification of validated biomarkers having significant clinical (i.e. diagnostic/prognostic) potential for the field of cancer biology. AVAILIBILITY: Neuroshell 2 is commercially available from ward systems.

L2 ANSWER 9 OF 46 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 2002:502832 BIOSIS
DN PREV200200502832
TI ProteinChip technology: A new and facile method for the identification and measurement of high-density lipoproteins apoA-I and apoA-II and their glycosylated products in patients with diabetes and cardiovascular disease.
AU Dayal, Bishambar (1); Ertel, Norman H. (1)
CS (1) VA NJ Health Care System, East Orange, NJ, 07018: bishambar.dayal@med.va.gov, norman.ertel@med.va.gov USA
SO Journal of Proteome Research, (July August, 2002) Vol. 1, No. 4, pp. 375-380. http://pubs.acs.org/JPR. print.
ISSN: 1535-3893.
DT Article
LA English
AB This paper describes a ProteinChip technology for the identification and quantification of apolipoprotein profiles in crude biological samples. Expression levels of apoA-I and apoA-II and their glycosylated products were accomplished using single 1 muL plasma samples. In the present studies, strong anionic and weak cationic exchanger ProteinChips (SAX2 and WCX2 chip surfaces) were tested, and the WCX2 chip was found to be selective for specific apolipoproteins. Using the WCX2 chip and analysis via surface-enhanced laser desorption ionization mass spectrometry (SELDI-MS), apoA-I and apoA-II were separated as sharp peaks at 28 and 17 kD and did not overlap with other serum protein peaks. Since these assays can be completed on a large number of clinical samples in approximately 1 h, further development of this technique will facilitate both epidemiological studies and therapeutic trials in assessing the role of the apolipoproteins and their glycosylated products in atherosclerosis.

L2 ANSWER 10 OF 46 MEDLINE DUPLICATE 4
AN 2002159816 MEDLINE
DN 21888704 PubMed ID: 11891524
TI Analysis of microdissected prostate tissue with ProteinChip arrays--a way to new insights into carcinogenesis and to diagnostic tools.
AU Wellmann Axel; Wollscheid Volker; Lu Hong; Ma Zhan Lu; Albers Peter;

Schutze Karin; Rohde Volker; Behrens Peter; Dreschers Stefan; Ko Yon; Wernert Nicolas

CS Institute of Pathology, University of Bonn, D-53127 Bonn, Germany.. axel.wellmann@uni.bonn.de

SO INTERNATIONAL JOURNAL OF MOLECULAR MEDICINE, (2002 Apr) 9 (4) 341-7. Journal code: 9810955. ISSN: 1107-3756.

CY Greece

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 200207

ED Entered STN: 20020314
Last Updated on STN: 20020718
Entered Medline: 20020717

AB Prostate carcinomas are one of the most common malignancies in western societies. The pathogenesis of this tumor is still poorly understood. These tumors present with two characteristic features: epithelial-mesenchymal interactions, which play a pivotal role for tumor development and most of clinically manifest cancers arise in prostate proper compared to a minority of tumors which develop in the transitional zone. Deciphering the epithelial-mesenchymal cross talk and identification of molecular pecularities of the sub-populations of cells in different zones can therefore help understanding carcinogenesis and development of new, non-invasive tools for the diagnosis and prognosis of prostate carcinomas which has remained a challenge until today. A ProteinChip array technology (SELDI = surface enhanced laser desorption ionization) has been developed recently by **Ciphergen** Biosystems enabling analysis and profiling of complex protein mixtures from a few cells. This study describes the analysis of approximately 500-1000 freshly obtained prostate cells by SELDI-TOF-MS (surface enhanced laser desorption ionization time-of-flight mass spectrometry). Pure cell populations of stroma, epithelium and tumor cells were selected by laser assisted microdissection. Multiple specific protein patterns were reproducibly detected in the range from 1.5 to 30 kDa in 28 sub-populations of 4 tumorous prostates and 1 control. A specific 4.3 kDa peak was increased in the prostate tumor stroma compared to normal prostate proper and transitional zone stroma and increased in prostate tumor glands compared to normal prostate proper and transitional zone glands. Coupling laser assisted microdissection with SELDI provides tremendous opportunities to identify cell and tumor specific proteins to understand molecular events underlying prostate carcinoma development. It underlines the vast potential of this technology to better understand pathogenesis and identify potential candidates for new specific biomarkers in general which could help to screen for and distinguish disease entities, i.e. between clinically significant and insignificant carcinomas of the prostate.

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     FILE 'MEDLINE, BIOSIS' ENTERED AT 13:32:50 ON 15 JUL 2003
L1            54 S CIPHERGEN
L2            46 DUPLICATE REMOVE L1 (8 DUPLICATES REMOVED)

=> s l2 and py<2001
L3             7 L2 AND PY<2001

=> d 1-7 bib ab

L3   ANSWER 1 OF 7     MEDLINE
AN   2001227489      MEDLINE
DN   21156490    PubMed ID: 11257925
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TI Recent trends in protein biochip technology.
AU Weinberger S R; Morris T S; Pawlak M
CS Ciphergen Biosystems, Inc., 6611 Dumbarton Circle, Fremont, CA 94555, USA.. sweinberger@ciphergen.com
SO Pharmacogenomics, **(2000 Nov)** 1 (4) 395-416. Ref: 128
Journal code: 100897350. ISSN: 1462-2416.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals
EM 200104
ED Entered STN: 20010502
Last Updated on STN: 20010502
Entered Medline: 20010426
AB This article presents current trends and advances in protein biochip technologies that rely upon extraction and retention of target proteins from liquid media. Analytical strengths as well as technical challenges for these evolving platforms are presented with particular emphasis on selectivity, sensitivity, throughput and utility in the post-genome era. A general review of protein biochip technology is provided, which delineates approaches for protein biochip format and operation, as well as protein detection. A focused discussion of three protein biochip technologies, Biomolecular Interaction Analysis (Biacore, Uppsala, Sweden), Surface Enhanced Laser Desorption/Ionisation (SELDI) ProteinChip Arrays (**Ciphergen** Biosystems, Fremont, CA, USA) and Fluorescent Planar Wave Guide (Zeptosens, Witterswil, Switzerland), follows along with examples of relevant applications.

L3 ANSWER 2 OF 7 MEDLINE
AN 2001223577 MEDLINE
DN 20496094 PubMed ID: 11043389
TI The ProteinChip System from **Ciphergen**: a new technique for rapid, micro-scale protein biology.
AU Davies H A
CS Ciphergen Biosystems Ltd., Surrey Technology Centre, Guildford, UK.. hdavies@ciphergen.com
SO JOURNAL OF MOLECULAR MEDICINE, **(2000)** 78 (7) B29.
Journal code: 9504370. ISSN: 0946-2716.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200104
ED Entered STN: 20010502
Last Updated on STN: 20010502
Entered Medline: 20010426

L3 ANSWER 3 OF 7 MEDLINE
AN 2000464053 MEDLINE
DN 20469098 PubMed ID: 11016883
TI The use of seldi proteinchip arrays to monitor production of Alzheimer's betaamyloid in transfected cells.
AU Austen B M; Frears E R; Davies H
CS Department of Surgery, St George's Hospital Medical School, London, UK.. sghk200@sghms.ac.uk
SO JOURNAL OF PEPTIDE SCIENCE, **(2000 Sep)** 6 (9) 459-69.
Journal code: 9506309. ISSN: 1075-2617.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200101

ED Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010125

AB beta-Amyloid (Abeta), a 39-43 residue peptide, is the principal component of senile plaques found in the brains of patients with Alzheimer's disease (AD). There are two main lines of evidence that its deposition is the cause of neurodegeneration. First, mutations found in three genes in familial Alzheimer's cases give rise to increased production of the longest, most toxic, form, Abeta 1-42. Second. aggregated Abeta is toxic to neuronal cells in culture. Inhibitors of the proteases involved in its release from the amyloid precursor protein are, therefore, of major therapeutic interest. The best candidates for the releasing proteases are both aspartyl proteases, which are integrated into the membranes of the endoplasmic reticulum and Golgi network. A sensitive assay using **Ciphergen**'s Seldi system has been developed to measure all the variants of Abeta in culture supernatants, which will be of great value in screening inhibitors of these proteases. With this assay, it has been shown that increasing intracellular cholesterol increases the activities of both beta-secretase, and gamma-secretase 42. Moreover, changing the intracellular targeting of amyloid precursor glycoprotein (APP) yields increased alpha-secretase cleavage, and increases in the amounts of oxidized/nitrated forms of Abeta.

L3 ANSWER 4 OF 7 MEDLINE
AN 2000097082 MEDLINE
DN 20097082 PubMed ID: 10631507
TI Profiling of amyloid beta peptide variants using SELDI Protein Chip arrays.
AU Davies H; Lomas L; Austen B
CS Ciphergen Biosystems, Surry, UK.
SO BIOTECHNIQUES, **(1999 Dec)** 27 (6) 1258-61.
Journal code: 8306785. ISSN: 0736-6205.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200002
ED Entered STN: 20000218
Last Updated on STN: 20000218
Entered Medline: 20000209

AB The profile of amyloid beta (A beta) peptide variants secreted into the media of human cultured cells that express the amyloid precursor protein was examined by Surface Enhanced Laser Desorption/Ionization (SELDI) ProteinChip technology from **Ciphergen** Biosystems using biologically active ProteinChip Arrays. An anti-A beta polyclonal antibody (anti-NTA4) was used to capture and purify multiple immunoreactive A beta fragments from a single microliter of media onto the ProteinChip Array. Fragments retained on the surface of the ProteinChip Array were detected directly by mass in the ProteinChip System to provide detailed information on the identity of different A beta variants secreted from the cultured cells. We discuss existing and potential applications of this immunoassay for the detection and relative quantitation of A beta species from both cultured cell systems and clinical samples.

L3 ANSWER 5 OF 7 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 2001:312003 BIOSIS
DN PREV200100312003
TI The application of protein chip surface-enhanced laser desorption/ionization (SELDI) mass spectrometry for the identification of proteins in chronic lymphocytic leukemia.
AU Czader, M. (1); Kuzdzal, S. (1); Flinn, I. (1); Byrd, J.; Chan, D. (1); Borowitz, M. J. (1)
CS (1) Johns Hopkins Medical Institutions, Baltimore, MD USA
SO Blood, (**November 16, 2000**) Vol. 96, No. 11 Part 1, pp. 579a.

print.
Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology
. ISSN: 0006-4971.

DT Conference
LA English
SL English
AB There is a scarcity of data on protein modifications related to the malignant behavior of hematologic malignancies including chronic lymphocytic leukemia (CLL). This is partly due to the technical difficulties in the purification and identification of small amounts of protein, which in contrast to nucleic acid, can not be readily amplified. SELDI mass spectrometry makes it possible to rapidly determine the molecular weights of sample proteins using as few as 2 X 105 cells. It provides femtomole-level sensitivity for proteins ranging from 1 to more than 300 kD. In addition, the identification of the protein can be accomplished on the same protein chip array on which the initial analysis was started. This technique has been used to identify unique protein markers in malignancies including prostate cancer. We applied SELDI to a series of cases of CLL and other lymphoproliferative disorders previously characterized by four color flow cytometry. These included 9 cases of classical CLL, 2 cases of atypical CLL expressing bright CD20 and/or CD79b but positive for CD5 and CD23, and 1 case of a CD5 negative B-cell lymphoproliferative disorder. Abnormal lymphocytes accounted for at least 90% of cells in all cases. Lysed whole blood specimens were extracted with triton X100 and applied to highly selective protein chips, washed under selective conditions, and analyzed by SELDI (**Ciphergen** Biosystems, Palo Alto, CA). Aliquots of either normal peripheral blood or flow-sorted CD19+ normal B cells were similarly treated. There were numerous protein peaks throughout the range 1-300kD that were common to all leukemic samples, normal peripheral blood and flow-sorted B-cells. In addition, however, there were three unique peaks of 11.3kD and 13.8kD and 14.0kD found only in the leukemic samples. The same unique proteins were seen with both non-polar and hydrophobic chips, and were common to all 9 CLL samples. They were also present in both cases of atypical CLL, and the CD5-negative lymphoproliferative disorder, indicating the similarity of these disorders and CLL. We conclude that SELDI technology may be used to screen for proteins that can distinguish B-cell lymphoproliferative disorders from normal blood and normal B cells. Investigation of new chip surfaces and use of additional wash conditions may reveal additional disease-associated markers. Further characterization of these unique proteins is underway to understand the role they may play in the pathogenesis of these disorders.

L3 ANSWER 6 OF 7 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 2001:49474 BIOSIS
DN PREV200100049474
TI Beyond the Human Genome.
AU Ezzell, Carol
SO Scientific American, (**July, 2000**) Vol. 283, No. 1, pp. 64-69.
print.
ISSN: 0036-8733.
DT Article
LA English
SL English

L3 ANSWER 7 OF 7 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 2000:483757 BIOSIS
DN PREV200000483757
TI A rapid protein profiling system that speeds study of cancer and other diseases.
AU Rubin, Richard B. (1); Merchant, Maggie (1)
CS (1) Ciphergen Biosystems, Inc., 6611 Dumbarton Cir., Fremont, CA, 94555

USA
SO American Biotechnology Laboratory, (**August, 2000**) Vol. 18, No. 9, pp. 18, 20. print.
ISSN: 0749-3223.
DT Article
LA English
SL English

=>

---Logging off of STN---

=>
Executing the logoff script...

=> LOG Y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	22.65	22.86

STN INTERNATIONAL LOGOFF AT 13:40:35 ON 15 JUL 2003